

A -

FIGURE 1

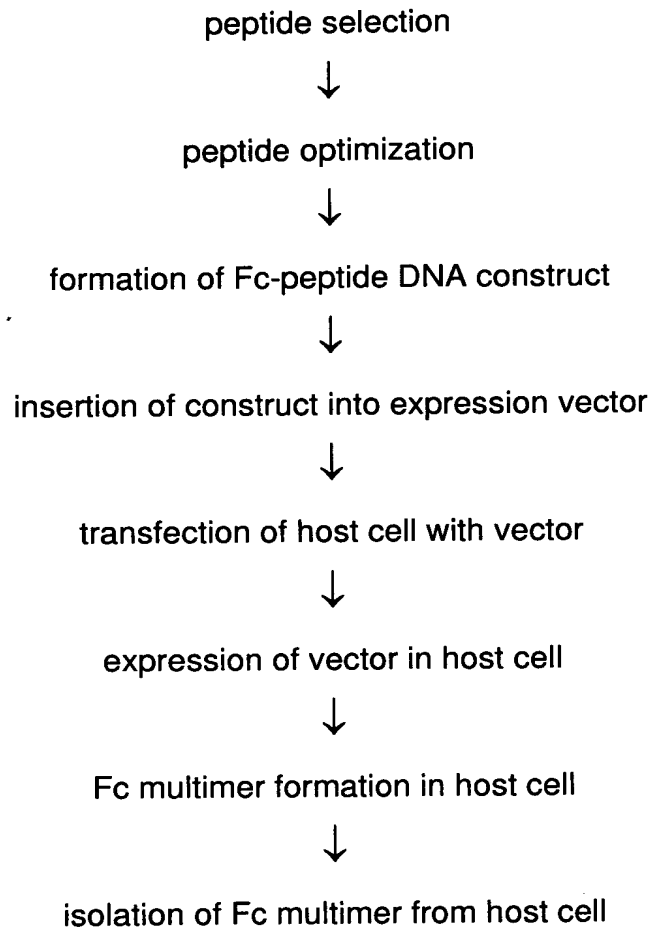


FIGURE 2

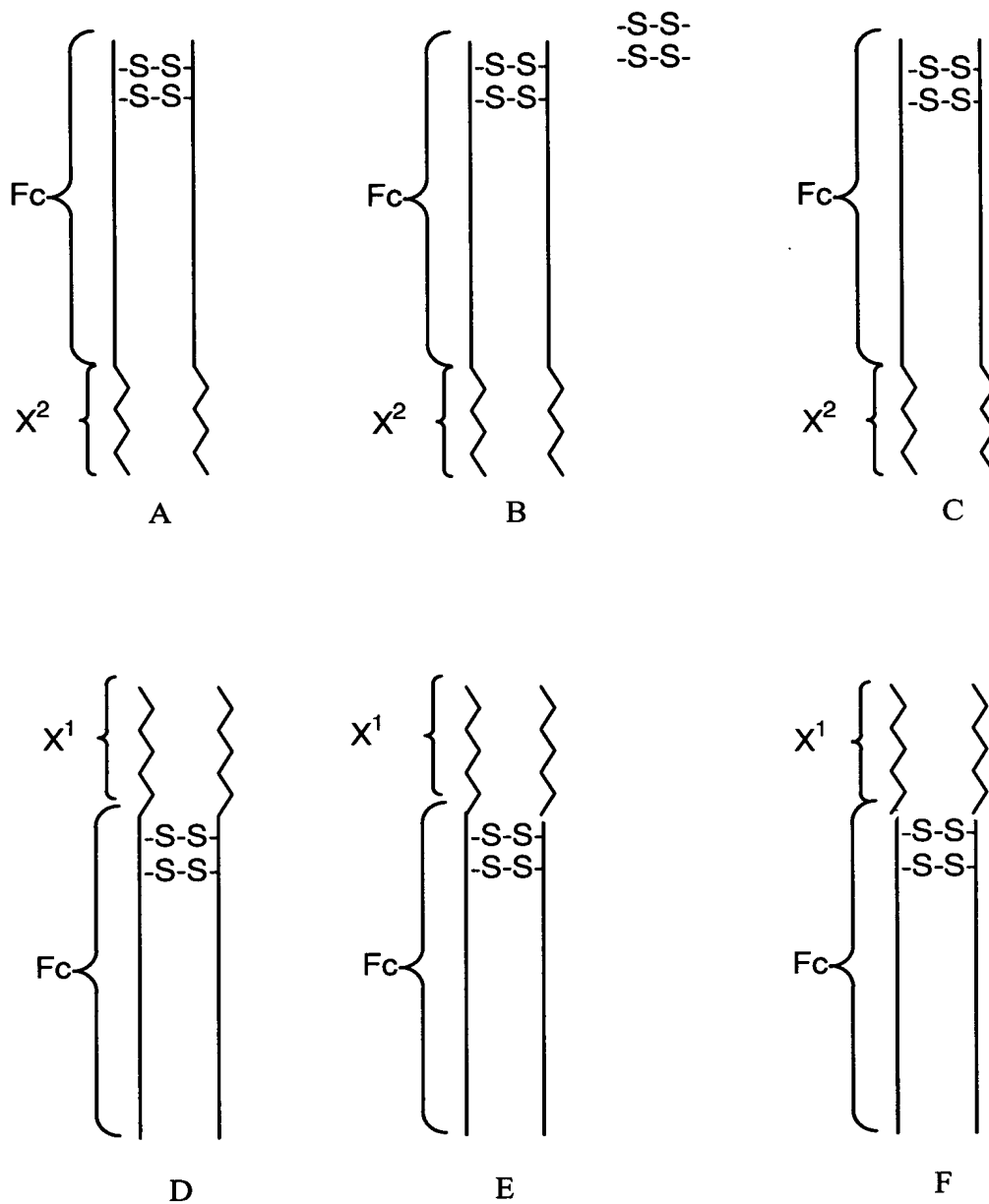


FIGURE 3

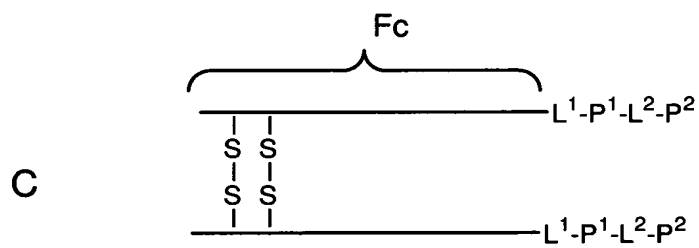
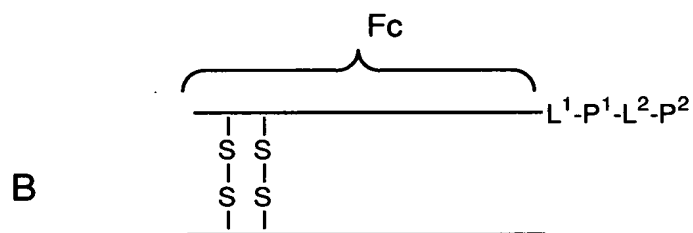
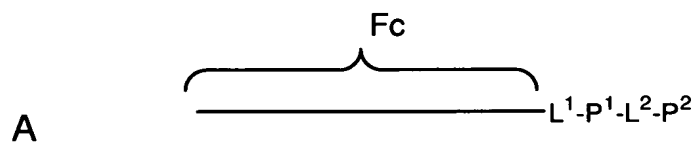


FIGURE 4

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ATGGACAAAACACACATGCCACCTTGTCAGCTCCGGAACCTCTGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a      M D K T H T C P P C P A P E L L G G P S -

61      GTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
-----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a      V F L F P P K P K D T L M I S R T P E V -

121     ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
-----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a      T C V V V D V S H E D P E V K F N W Y V -

181     GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
-----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTGTC

a      D G V E V H N A K T K P R E E Q Y N S T -

241     TACCGTGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
-----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATG

a      Y R V V S V L T V L H Q D W L N G K E Y -

301     AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
-----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a      K C K V S N K A L P A P I E K T I S K A -

361     AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACC
-----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a      K G Q P R E P Q V Y T L P P S R D E L T -

421     AAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
-----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a      K N Q V S L T C L V K G F Y P S D I A V -

481     GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGAC
-----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGACACGACCTG

a      E W E S N G Q P E N N Y K T T P P V L D -

541     TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
-----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a      S D G S F F L Y S K L T V D K S R W Q Q -

601     GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
-----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC

a      G N V F S C S V M H E A L H N H Y T Q K -

661     AGCCTCTCCCTGTCTCCGGGTAAA
-----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

a      S L S L S P G K

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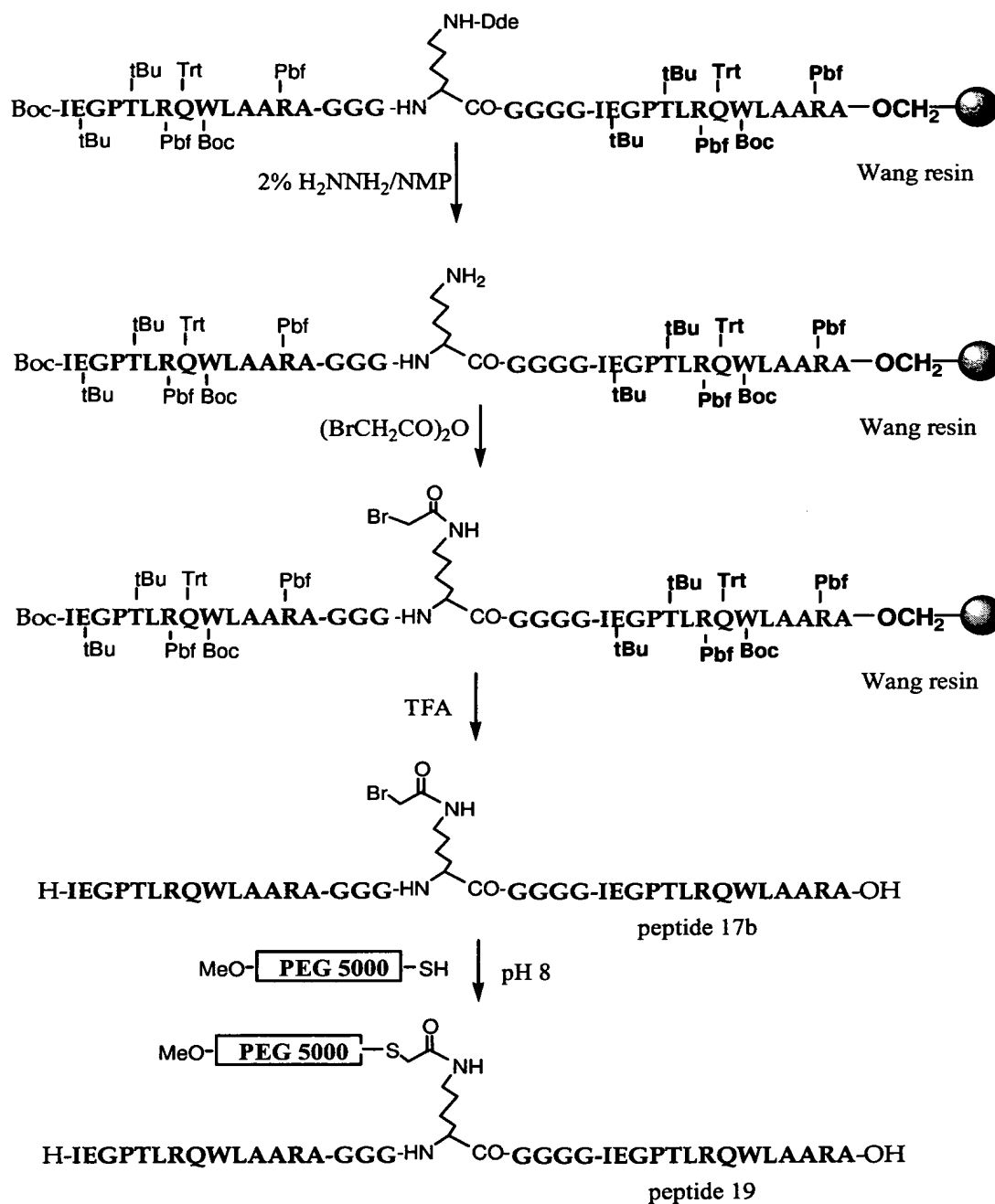
FIGURE 5

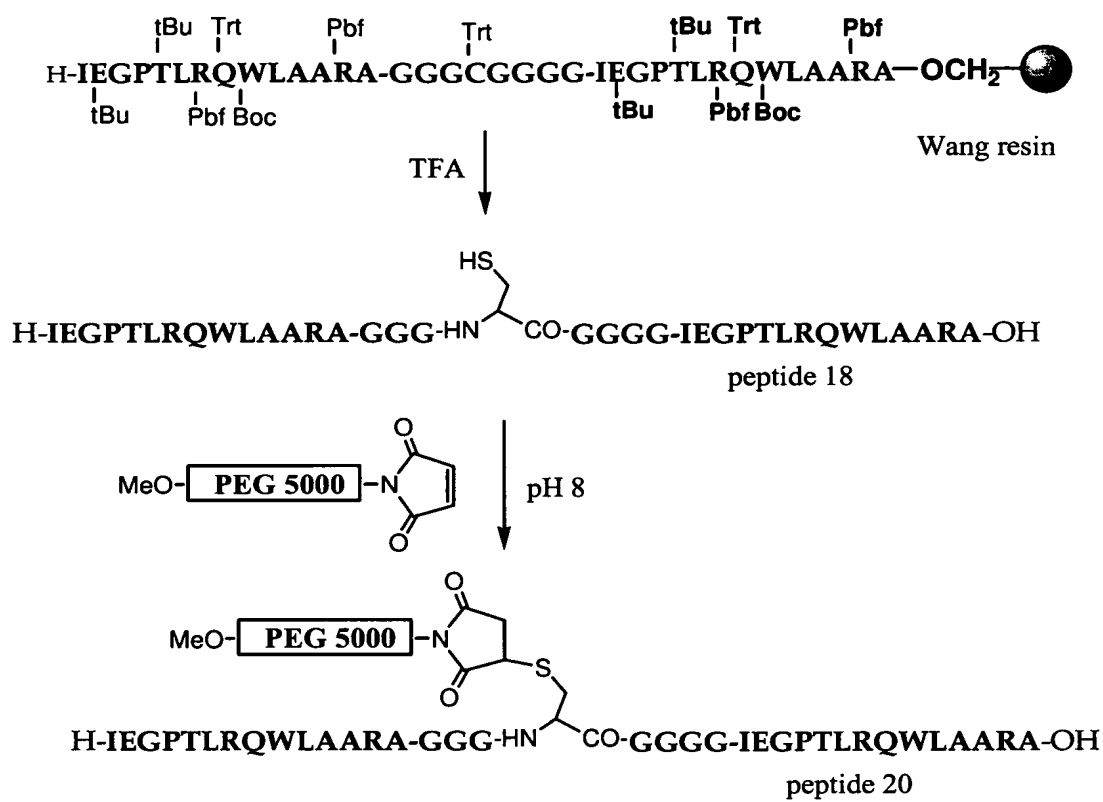
FIGURE 6

FIGURE 7

XbaI
|
TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGGACAAAACACACATGTC
1 -----+-----+-----+-----+-----+-----+-----+ 60
AGATCTAAACAAAATTGATTAATTTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG
c M D K T H T C P -

CACCTTGTCAGCTCCGGAACCTCGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC
61 -----+-----+-----+-----+-----+-----+-----+ 120
GTGGAACAGGTCGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG
c P C P A P E L L G G P S V F L F P P K P -

CCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGGACGTGA
121 -----+-----+-----+-----+-----+-----+-----+ 180
GGTTCCTGTGGGAGTACTAGAGGCCTGGGGACTCCAGTGTACGCACCACCACGTGCACT
c K D T L M I S R T P E V T C V V V D V S -

GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
181 -----+-----+-----+-----+-----+-----+-----+ 240
CGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
c H E D P E V K F N W Y V D G V E V H N A -

CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCA
241 -----+-----+-----+-----+-----+-----+-----+ 300
GGTTCCTGTTTCGGGCCCCCTCTCGTCATGTTGTCGTGCATGGCACACCAGTCGGAGGAGT
c K T K P R E E Q Y N S T Y R V V S V L T -

CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
301 -----+-----+-----+-----+-----+-----+-----+ 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATGTTCCAGAGGTGTTTC
c V L H Q D W L N G K E Y K C K V S N K A -

CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCAAAGGGCAGCCCCGAGAACCAC
361 -----+-----+-----+-----+-----+-----+-----+ 420
GGGAGGGTGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTTGGTG
c L P A P I E K T I S K A K G Q P R E P Q -

AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
421 -----+-----+-----+-----+-----+-----+-----+ 480
TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
c V Y T L P P S R D E L T K N Q V S L T C -

GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
481 -----+-----+-----+-----+-----+-----+-----+ 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
c L V K G F Y P S D I A V E W E S N G Q P -

CGGAGAACAACATAAGACCACGCCCTCCCGTGTGACTCCGACGGCTCTTCTCTCTCT
541 -----+-----+-----+-----+-----+-----+-----+ 600
GCCCTCTGTTGATGTTCTGGTGGGAGGGCAGCACCTGAGGCTGCCGAGGAAGAAGGAGA
c E N N Y K T T P P V L D S D G S F F L Y -

ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
601 -----+-----+-----+-----+-----+-----+-----+ 660
TGTGCTTCGAGTGGCACCTGTTCTCTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
c S K L T V D K S R W Q Q G N V F S C S V -

TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTA
661 -----+-----+-----+-----+-----+-----+-----+ 720
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCAT
c M H E A L H N H Y T Q K S L S L S P G K -

AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCT
721 -----+-----+-----+-----+-----+-----+-----+ 780
TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGAGCACGAA
c G G G G G I E G P T L R Q W L A A R A * -

BamHI
|
AATCTCGAGGATCC
781 -----+----- 794
TTAGAGCTCCTAGG

FIGURE 8

XbaI
 |
 1 TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60
 AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
 M D K T H T C P -
 c
 61 CACCTTGTCCAGCTCCGGAACCTCGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAAC 120
 GTGGAACAGGTCGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG
 P C P A P E L L G G P S V F L F P P K P -
 c
 121 CCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA 180
 GGTTCCTGTGGGAGTACTAGAGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
 K D T L M I S R T P E V T C V V V D V S -
 c
 181 GGCACGAAGACCCCTGAGGTCAAGTCAACTGGTACGTGGACGCGTGGAGGTGCATAATG 240
 CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
 H E D P E V K F N W Y V D G V E V H N A -
 c
 241 CCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCTCA 300
 GGTTCCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGGAGGAGT
 K T K P R E E Q Y N S T Y R V V S V L T -
 c
 301 CCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG 360
 GGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTACGTTCCAGAGGTGTTTTC
 V L H Q D W L N G K E Y K C K V S N K A -
 c
 361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGCGAGCCCCGAGAACCAC 420
 GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
 L P A P I E K T I S K A K G Q P R E P Q -
 c
 421 AGGTGTACACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCCTGACCT 480
 TCACATATGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGA
 V Y T L P P S R D E L T K N Q V S L T C -
 c
 481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
 CGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
 L V K G F Y P S D I A V E W E S N G Q P -
 c
 541 CGGAGAACAACATAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTCT 600
 GCCTCTTGTGATGTTCTGGTGGGAGGGCAGCACCTGAGGCTGCCGAGGAAGAAGGAGA
 E N N Y K T T P V L D S D G S F F L Y -
 c
 601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660
 TGTGCTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
 S K L T V D K S R W Q Q G N V F S C S V -
 c
 661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720
 ACTACGTACTCCGAGACGTGTTGGTGTGTGCGTCTTCTCGGAGAGGGACAGAGCCCAT
 M H E A L H N H Y T Q K S L S L S P G K -
 c
 721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAAGTGGCTGGCTGCTCGTGCTG 780
 TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGACGACGAC
 G G G G G I E G P T L R Q W L A A R A G -
 c
 781 GTGGTGGAGGTGGCGGGGAGGTATTGAGGGCCCAACCCCTTCGCCAATGGCTTGACGAC 840
 CACCACCTCCACCGCCGCTCCATAACTCCCGGTTGGGAAGCGGTTACCGAAGCTCGTG
 G G G G G G I E G P T L R Q W L A A R -
 c
 BamHI
 |
 841 GCGCATAATCTCGAGGATCCG 861
 CGCGTATTAGAGCTCCTAGGC
 c A * -

FIGURE 9

XbaI
|
1 TCTAGATTGTTTTAACTAATTAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC 60
-----+-----+-----+-----+-----+
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATAC TAGCTTCAGGCTGAGACG
M I E G P T L R -

c

61 GTCAGTGGCTGGCTGCTCGTGCTGGCGGTGGTGGCGGAGGGGGTGGCATTGAGGGCCCAA 120
-----+-----+-----+-----+-----+
CAGTCACCGACCGACGAGCAGCAGCCGCCACCACCGCCTCCCCACCGTAACCTCCGGGTT
Q W L A A R A G G G G G G G G I E G P T -

c

121 CCCTTCGCCAATGGCTTGCAGCACGCGCAGGGGGAGGCGGTGGGGACAAAACCTCACACAT 180
-----+-----+-----+-----+-----+
GGGAAGCGGTTACCGAACGTCGTGCGCGTCCCTCCGCCACCCCTGTTTGTAGTGTGTA
L R Q W L A A R A G G G G G G D K T H T C -

c

181 GTCCACCTTGCCCCAGCACCTGAACCTCTGGGGGACCGTCAGTTTCTCTTCCCCCAA 240
-----+-----+-----+-----+-----+
CAGGTGGAACGGGTTCGTGACTTGAGGACCCCTCGCAGTCAAAGGAGAAGGGGGTT
P P C P A P E L L G G P S V F L F P P K -

c

241 AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACG 300
-----+-----+-----+-----+-----+
TTGGGTTCTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACTGC
P K D T L M I S R T P E V T C V V V D V -

c

301 TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA 360
-----+-----+-----+-----+-----+
ACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTAT
S H E D P E V K F N W Y V D G V E V H N -

c

361 ATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC 420
-----+-----+-----+-----+-----+
TACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCGTGCATGGCACACCAGTCGCAGG
A K T K P R E E Q Y N S T Y R V V S V L -

c

421 TCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA 480
-----+-----+-----+-----+-----+
AGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCCTCATGTTACAGTCCAGAGGTTGT
T V L H Q D W L N G K E Y K C K V S N K -

c

481 AAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAAC 540
-----+-----+-----+-----+-----+
TTCGGGAGGGTCGGGGGTAGCTCTTTGTGAGAGGTTTCGGTTTCCCGTCGGGGCTCTTG
A L P A P I E K T I S K A K G Q P R E P -

c

541 CACAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACAGCTGA 600
-----+-----+-----+-----+-----+
GTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACT
Q V Y T L P P S R D E L T K N Q V S L T -

c

601 CCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC 660
-----+-----+-----+-----+-----+
GGACGGACCAAGTTTCCGAAGATAGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCG
C L V K G F Y P S D I A V E W E S N G Q -

c

661 AGCCGGAGAACAATAACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCC 720
-----+-----+-----+-----+-----+
TCGGCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGG
P E N N Y K T T P P V L D S D G S F F L -

c

721 TCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCT 780
-----+-----+-----+-----+-----+
AGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGA
Y S K L T V D K S R W Q Q G N V F S C S -

c

781 CCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGG 840
-----+-----+-----+-----+-----+
GGCACTACTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCC
V M H E A L H N H Y T Q K S L S L S P G -

c

BamHI
|
841 GTAAATAATGGATCC 855
-----+-----
CATTTATTACCTAGG
K *

FIGURE 10

XbaI
|
1 TCTAGATTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC 60
-----+-----+-----+-----+-----+-----+
AGATCTAAACAAAATTGATTAATTTCTCTCTATTGTATACTAGCTTCCAGGCTGAGACG
c M I E G P T L R -

61 GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCGGTGGGGACAAAACACACATGTCCAC 120
-----+-----+-----+-----+-----+-----+
c CAGTCCACCGACCGACGAGCAGCAGCACCCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG
Q W L A A R A G G G G G D K T H T C P P -

121 CTGCCCAGCACCTGAACCTCTGGGGGACCGTCAGTTTTCTCTTCCCCCAAAACCCA 180
-----+-----+-----+-----+-----+-----+
c GAACGGGTCGTGGACTTGAGGACCCCTGGCAGTCAAAGGAGAAGGGGGTTTGGGT
C P A P E L L G G P S V F L F P P K P K -

181 AGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCC 240
-----+-----+-----+-----+-----+-----+
c TCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGTACGCACCACCTGCACTCGG
D T L M I S R T P E V T C V V V D V S H -

241 ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA 300
-----+-----+-----+-----+-----+-----+
c TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT
E D P E V K F N W Y V D G V E V H N A K -

301 AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACC G 360
-----+-----+-----+-----+-----+-----+
c TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTGTCATGGCACACCAGTCGCAGGAGTGGC
T K P R E E Q Y N S T Y R V V S V L T V -

361 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC 420
-----+-----+-----+-----+-----+-----+
c AGGACGTGGTCTGACCGACTTACCGTTCCCTCATGTTACGTTCCAGAGGTGTTTCGGG
L H Q D W L N G K E Y K C K V S N K A L -

421 TCCCAGCCCCCATCGAGAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGG 480
-----+-----+-----+-----+-----+-----+
c AGGGTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC
P A P I E K T I S K A K G Q P R E P Q V -

481 TGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCC 540
-----+-----+-----+-----+-----+-----+
c ACATGTGGGAGCGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGACGG
Y T L P P S R D E L T K N Q V S L T C L -

541 TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG 600
-----+-----+-----+-----+-----+-----+
c ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCC
V K G F Y P S D I A V E W E S N G Q P E -

601 AGAACAACCTACAAGACCACGCTCCCGTGGTGGACTCCGACGGCTCCTTCTCTCTACA 660
-----+-----+-----+-----+-----+-----+
c TCTTGTGATGTTCTGGTGGGAGGGCAGCAGCTGAGGCTGCCGAGGAAGAAGGAGATGT
N N Y K T T P P V L D S D G S F F L Y S -

661 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGA 720
-----+-----+-----+-----+-----+-----+
c CGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACT
K L T V D K S R W Q Q G N V F S C S V M -

721 TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT 780
-----+-----+-----+-----+-----+-----+
c ACGTACTCCGAGACGTGTTGGTGTATGTCGTCTTCTCGGAGAGGGACAGAGGCCATTTA
H E A L H N H Y T Q K S L S L S P G K * -

BamHI
|
AATGGATCC
781 ----- 789
TTACCTAGG

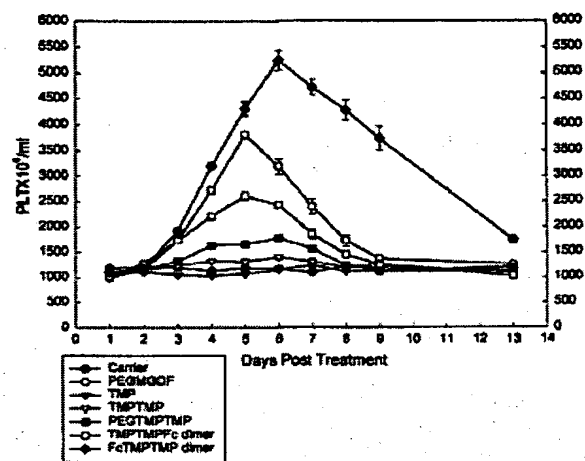
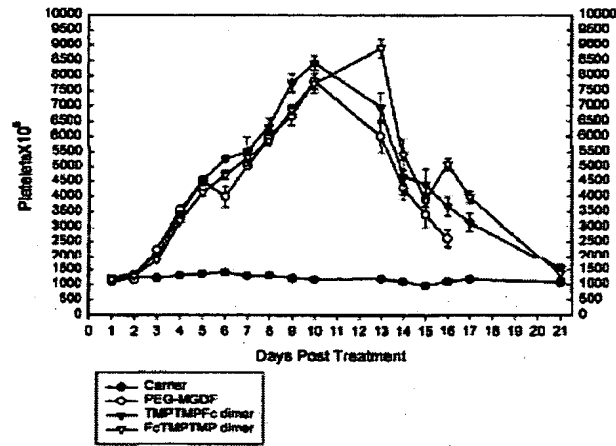
FIGURE 11

FIGURE 12

BamHI

[illegible]

BamHI

XbaI
|
TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC
1 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 60
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTCCATGAATGAGAACGG
M G G T Y S C H -

61 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 120
ACTTCGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGCGGGGGGACA
TGAAGCCGGGGGCGACTGAACCCATACATTCCGGTGTCCCCCACCCTCCGCCCCCCTGT
F G P L T W V C K P Q G G G G G G G D K -

121 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 180
AAACTCACACATGTCCACCTTGCCACGACCTGAACTCCTGGGGGACCGTCAGTTTTTC
TTTGAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCCCTGGCAGTCAAAGG
T H T C P P C P A P E L L G G P S V F L -

181 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 240
TCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCG
AGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGTACGC
F P P K P K D T L M I S R T P E V T C V -

241 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 300
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG
ACCACCACCTCGACTCGGTCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
V V D V S H E D P E V K F N W Y V D G V -

301 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 360
TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
ACCTCCACGTATTACGGTCTCTGTTTCGGCGCCCTCTCGTCATGTTGTCTGTCATGGCAC
E V H N A K T K P R E E Q Y N S T Y R V -

361 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 420
TGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
ACCAGTCGACAGGAGTGGCAGGACGTGGTCTGACCGACTTACCCTTCTCATGTTACCGT
V S V L T V L H Q D W L N G K E Y K C K -

421 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 480
AGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGC
TCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGTCTCTTTGGTAGAGGTTTCGGTTTCCCG
V S N K A L P A P I E K T I S K A K G Q -

481 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 540
AGCCCCGAGAACACAGGTGTACACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACC
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGG
P R E P Q V Y T L P P S R D E L T K N Q -

541 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 600
AGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
TCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCTGTAGCGGCACCTCACCC
V S L T C L V K G F Y P S D I A V E W E -

601 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 660
AGAGCAATGGGCAGCCGAGAAACAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACG
TCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGC
S N G Q P E N N Y K T T P P V L D S D G -

661 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 720
GCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
CGAGGAAGAAGGAGATGTCGTTCCAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGC
S F F L Y S K L T V D K S R W Q Q G N V -

721 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 780
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCT
AGAAGAGTACAGGACCTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA
F S C S V M H E A L H N H Y T Q K S L S -

BamHI
|
CCCTGTCTCCGGGTAAATAATGGATCC
781 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 807
GGGACAGAGGCCATTATACCTAGG
L S P G K *

FIGURE 15

XbaI
|
TCTAGATTTGAGTTTAACTTTTAGAAGGAGGAATAAAATATGGGAGGTACTTACTCTTG
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
AGATCTAAACTCAAATGAAAATCTTCCTCCTATTATTTATACCTCCATGAATGAGAAC
b M G G T Y S C -

CCACTTCGGCCCACTGACTTGGGTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGG
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
GGTGAAGCCGGGTGACTGAACCCAAACGTTTGGCGTCCCACCGCCGCCCGCCGCCACC
b H F G P L T W V C K P Q G G G G G G G G -

TACCTATTCTGTCTATTTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGTGGGG
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
ATGGATAAGGACAGTAAAACCGGGGCTGACCTGGACCCATACATTCGGTGTTCCTCCACCCCC
b T Y S C H F G P L T W V C K P Q G G G -

AGGCGGGGGGACAAAACCTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGG
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
TCCGCCCCCCTGTTTTGGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCC
b G G G D K T H T C P P C P A P E L L G G -

ACCGTCAGTTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCC
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
TGGCAGTCAAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCTGGGG
b P S V F L F P P K P K D T L M I S R T P -

TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTG
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
ACTCCAGTGTACGACACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC
b E V T C V V V D V S H E D P E V K F N W -

GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
CATGCACCTGCCGACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTT
b Y V D G V E V H N A K T K P R E E Q Y N -

CAGCACGTACCGTGTGGTCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAATAAACCATCTC
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
GTCTGTCATGGACACACAGTCCGAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTT
b S T Y R V V S V L T V L H Q D W L N G K -

GGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAATAAACCATCTC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
CCTCATGTTCAAGTCCAGAGGTTGTTTCGGGAGGGTGGGGGTAGCTCTTTTGGTAGAG
b E Y K C K V S N K A L P A P I E K T I S -

CAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGA
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
GTTTCGGTTTCCCTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACT
b K A K G Q P R E P Q V Y T L P P S R D E -

GCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
CGACTGGTCTTGGTCCAGTCCGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTA
b L T K N Q V S L T C L V K G F Y P S D I -

CGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGT
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
GCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCA
b A V E W E S N G Q P E N N Y K T T P P V -

GCTGGACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
CGACCTGAGGCTGCCGAGGAAGAAGGAGATGCGTTGAGTGGCACCTGTTCTCGTCCAC
b L D S D G S F F L Y S K L T V D K S R W -

GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
CGTCGTCCCCTTGAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTG
b Q Q G N V F S C S V M H E A L H N H Y T -

BamHI
|
GCAGAAGAGCCTCTCCCTGTCTCCGGTAAATAATGGATCC
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 881
CGTCTTCTCGGAGGGGACAGAGGCCATTTATTACCTAGG
b Q K S L S L S P G K *

[illegible]

FIGURE 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTCCGAGTCAGCTTCTGA-

-GGGCCTTTCTGTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
-CCCGGAAAGCAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG-

-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG-
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCCTCCACCGCCCGTCTGCGGGCG-

-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCTGACGGATGGCCTTTTTCGCGT-
-GTATTTGACGGTCCGTAGTTTAATTCGCTCTCCGGTAGGACTGCCTACCGGAAAAACGCA-

AatII
-TTCTACAACTCTTTTGTATTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-
-AAGATGTTTGAGAAAACAAATAAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-

-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAATGCTTTAGAAATACTTTGGCAGC-
-AAAATTTTATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-

-GGTTTGTGTTATGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC-
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTTACTGGCAGCGCAATG-

-TACAGCCTAATATTTTGAATATCCCAAGAGCTTTTTCCTTCGCATGCCACGCTAAAC-
-ATGTCGGATTATAAAAACTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTG-

-ATTCTTTTCTCTTTTGGTTAAATCGTTGTTTGAATTTATTTTGTATATTTATTTTTC-
-TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAAG-

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAATAATA-
-CTATTAATAGTTGATCTCTTCTTGTAAATTACCATAACAAGTATGTGCGTACATTTTAT-

-AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT-
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTGTATTCGTAAGGCTTCGGTAATA-

-TAGCAGTATGAATAGGGAACTAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA-
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-

-TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG-
-AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC-

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-

-AATATTGCCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-
-TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACCTTATAGTCTAAATTGGTATC-

-AATGAGGATAAATGATCGCGAGTAAATAATATTACAATGTACCATTTTAGTCATATCAG-
-TTACTCCTATTTACTAGCGCTCATTTATATAAGTGTACATGGTAAATCAGTATAGTC-

-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-
-TATTCGTAACCTAATTATAGTAATAACGAAGATGTCCGAAATTAAAAATAATTAATAAGACA-

-AAGTGTGTCGTCGCATTTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTG-
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-

-GCAAGTTTTGCGTGTTATATATCATTTAAACGGTAATAGATTGACATTTGATTCTAATAA-
-CGTTCAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAACTAAGATTATT-

FIGURE 17B

- ATTGGATTTTTGTCACACTATTATATCGCTTGAAATACAATTGTTTAAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -

- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -
- ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -

- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -
- GATCTAAACAAAATTGATTAATTTCTCTTATTGTATACCAATTGCGCAACCTTAAGCT -

- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -

- GAAGAAGAAGAAGAAAGCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTCTTTTCGGGCTTTCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -

- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -

- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIGURE 18

Erythroid parameters EMP-Fc, single bolus injection.

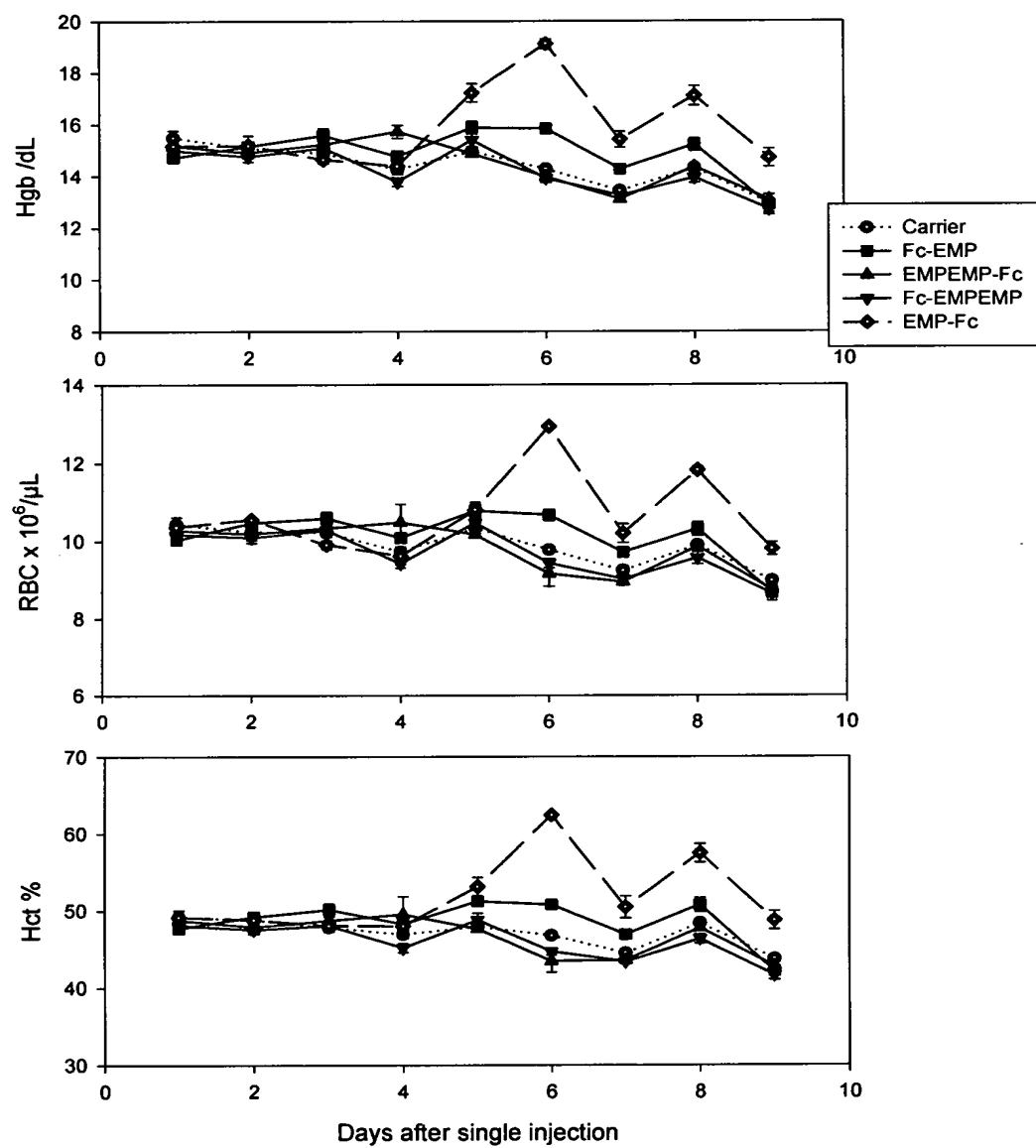


FIGURE 19

Normal female BDF1 mice treated with 100ug/kg EMP-Fc
in 7-day micro osmotic pumps

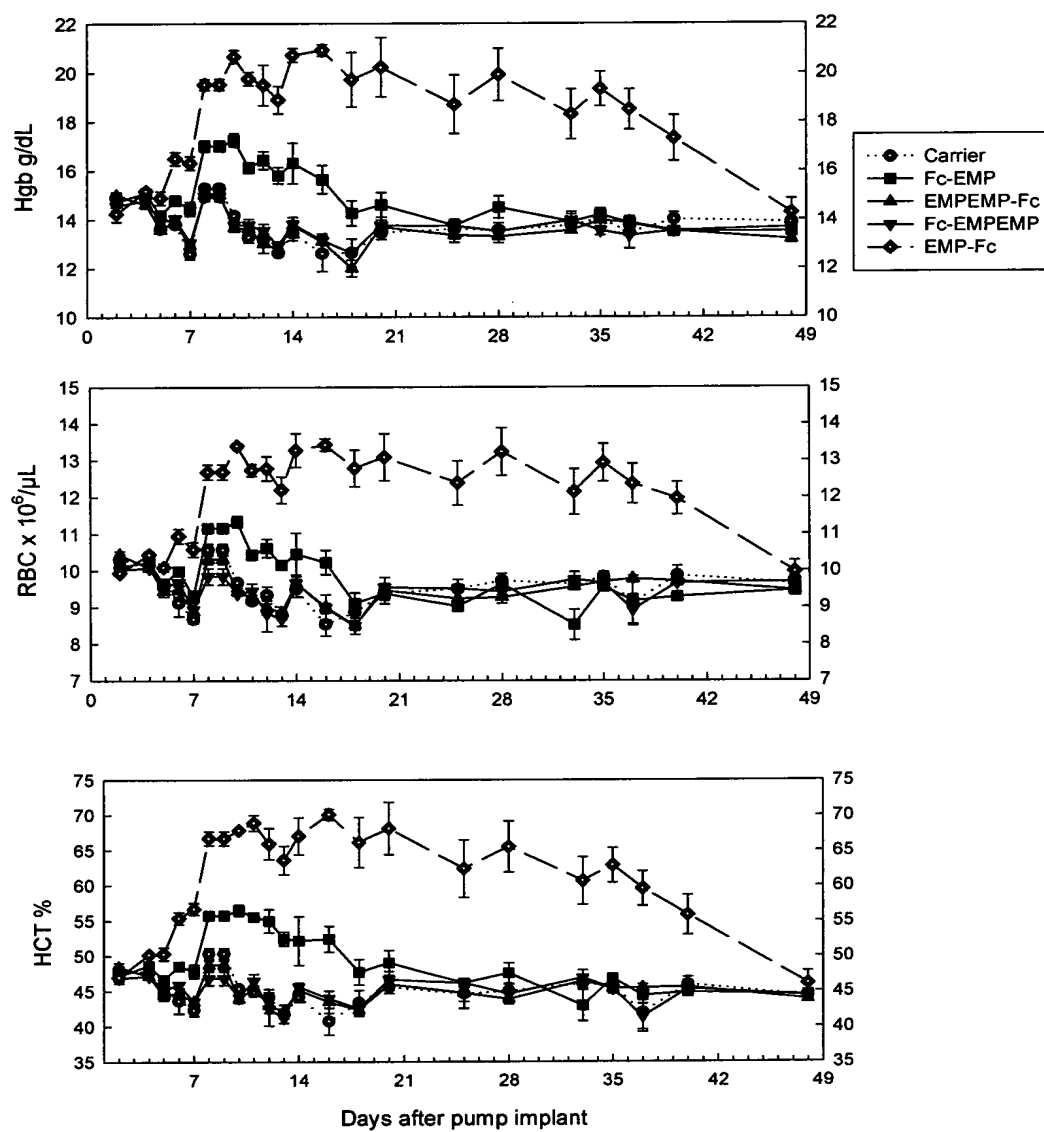


FIGURE 19A

NdeI
|
1 CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG 60
-----+-----+-----+-----+-----+-----+-----+
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
61 TCAGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
-----+-----+-----+-----+-----+-----+-----+
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
-----+-----+-----+-----+-----+-----+-----+
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
-----+-----+-----+-----+-----+-----+-----+
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG
a V D G V E V H N A K T K P R E E Q Y N S -
241 ACGTACCGTGTGGTCAGCGTCCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
-----+-----+-----+-----+-----+-----+-----+
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
-----+-----+-----+-----+-----+-----+-----+
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
-----+-----+-----+-----+-----+-----+-----+
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
421 ACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
-----+-----+-----+-----+-----+-----+-----+
TGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG 540
-----+-----+-----+-----+-----+-----+-----+
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCAGGAGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
541 GACTCCGACGGCTCCTTCTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
-----+-----+-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIGURE 19B

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+-----+
GTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC 720
-----+-----+-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a K S L S L S P G K G G G G G D F L P H Y -

BamHI
|

721 AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC 757
-----+-----+-----+-----+-----+
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a K N T S L G H R P *

FIGURE 20A

NdeI
|
CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTCACCGTCCGGGTGGAGGC
1 -----+-----+-----+-----+-----+-----+ 60
GTATACCTGAAGGACGGCGTGATGTTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG

a M D F L P H Y K N T S L G H R P G G G -

GGTGGGGACAAAACACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
61 -----+-----+-----+-----+-----+-----+ 120
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC

a G G D K T H T C P P C P A P E L L G G P -

TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG
121 -----+-----+-----+-----+-----+-----+ 180
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
181 -----+-----+-----+-----+-----+-----+ 240
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
241 -----+-----+-----+-----+-----+-----+ 300
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
301 -----+-----+-----+-----+-----+-----+ 360
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCA
361 -----+-----+-----+-----+-----+-----+ 420
ATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
421 -----+-----+-----+-----+-----+-----+ 480
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
481 -----+-----+-----+-----+-----+-----+ 540
TGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACTACAAGACCACGCCTCCCGTGCTG
541 -----+-----+-----+-----+-----+-----+ 600
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCAGCAG

a V E W E S N G Q P E N N Y K T T P P V L -

FIGURE 20B

```

601  GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAG
      -----+-----+-----+-----+-----+-----+ 660
      CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a    D S D G S F F L Y S K L T V D K S R W Q -

      CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661  -----+-----+-----+-----+-----+-----+ 720
      GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a    Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
      AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
721  -----+-----+-----+-----+-----+-----+ 761
      TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a    K S L S L S P G K *
```

a
b
c
d
e
f
g
h
i
j
k
l
m
n
o
p
q
r
s
t
u
v
w
x
y
z

FIGURE 21A

NdeI
|
1 CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG 60
-----+-----+-----+-----+-----+
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
-----+-----+-----+-----+-----+
AGTCAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
-----+-----+-----+-----+-----+
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
-----+-----+-----+-----+-----+
CACCTGCCGCACCTCCACGTATTACGGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
-----+-----+-----+-----+-----+
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
-----+-----+-----+-----+-----+
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCCGGGATGAGCTG 420
-----+-----+-----+-----+-----+
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
-----+-----+-----+-----+-----+
TGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGCTG 540
-----+-----+-----+-----+-----+
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIGURE 21B

```

601  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a    Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661  AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a    K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  -

                                     BamHI
                                     |
721  TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a    Y  W  Q  P  Y  A  L  P  L  *

```

601 660 720 763

FIGURE 22A

NdeI
|
CATATGTTTGAATGGACCCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG

a M F E W T P G Y W Q P Y A L P L G G G -

GGTGGGGACAAAACCTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
61 -----+-----+-----+-----+-----+-----+-----+ 120
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC

a G G D K T H T C P P C P A P E L L G G P -

TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG
121 -----+-----+-----+-----+-----+-----+-----+ 180
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
241 -----+-----+-----+-----+-----+-----+-----+ 300
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
301 -----+-----+-----+-----+-----+-----+-----+ 360
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCCGGATGAGCTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
481 -----+-----+-----+-----+-----+-----+-----+ 540
TGTTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

FIGURE 22B

```

601  GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
      -----+-----+-----+-----+-----+-----+ 660
      CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a    D S D G S F F L Y S K L T V D K S R W Q -

      CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661  -----+-----+-----+-----+-----+-----+ 720
      GTCCCCTTGACAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a    Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
      AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721  -----+-----+-----+-----+-----+ 757
      TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a    K S L S L S P G K *

```

601 660 720 757

FIGURE 23A

NdeI
|
CATATGGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACCTCTGGGGGGACCG
1 -----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG
-----+-----+-----+-----+-----+-----+ 120
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
-----+-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
-----+-----+-----+-----+-----+-----+ 360
ATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
-----+-----+-----+-----+-----+-----+ 480
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
-----+-----+-----+-----+-----+-----+ 540
CACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCAGGAGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

[illegible]

a

FIGURE 24A

NdeI
|
CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA

a M V E P N C D I H V M W E W E C F E R -

CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCCAGCACCTGAACTC
61 -----+-----+-----+-----+-----+-----+-----+ 120
GACCCACCACCACCACCACTGTTTTGAGTGTGTACAGGTGGCACGGGTTCGTGGACTTGAG

a L G G G G G D K T H T C P P C P A P E L -

CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCC
121 -----+-----+-----+-----+-----+-----+-----+ 180
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG

a L G G P S V F L F P P K P K D T L M I S -

CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
181 -----+-----+-----+-----+-----+-----+-----+ 240
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC

a R T P E V T C V V V D V S H E D P E V K -

TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC

a F N W Y V D G V E V H N A K T K P R E E -

CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
301 -----+-----+-----+-----+-----+-----+-----+ 360
GTCATGTTGTCTGTCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTCTGACCGAC

a Q Y N S T Y R V V S V L T V L H Q D W L -

AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTACCGTTCTCATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT

a N G K E Y K C K V S N K A L P A P I E K -

ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG

a T I S K A K G Q P R E P Q V Y T L P P S -

CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
481 -----+-----+-----+-----+-----+-----+-----+ 540
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGG

a R D E L T K N Q V S L T C L V K G F Y P -

AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACG
541 -----+-----+-----+-----+-----+-----+-----+ 600
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC

a S D I A V E W E S N G Q P E N N Y K T T -

FIGURE 24B

```

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG
-----+-----+-----+-----+-----+-----+ 660
GGAGGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTC

a   P P V L D S D G S F F L Y S K L T V D K -

661 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
-----+-----+-----+-----+-----+-----+ 720
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG

a   S R W Q Q G N V F S C S V M H E A L H N -

                                     BamHI
                                     |
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
-----+-----+-----+-----+-----+----- 773
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG

a   H Y T Q K S L S L S P G K *
```

CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG

FIGURE 25A

NdeI
|
1 CATATGGACAAAACCTCACACATGTCCACCTTGTCAGCTCCGGAACCTCTGGGGGGACCG 60
-----+-----+-----+-----+-----+
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
-----+-----+-----+-----+-----+
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
-----+-----+-----+-----+-----+
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
-----+-----+-----+-----+-----+
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGCG

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCCTACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
-----+-----+-----+-----+-----+
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCCTGACCGACTTACCGTTCCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
-----+-----+-----+-----+-----+
ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCCGGGATGAGCTG 420
-----+-----+-----+-----+-----+
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
-----+-----+-----+-----+-----+
TGGTTCTTGGTCCAGTCGGAAGTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGCTG 540
-----+-----+-----+-----+-----+
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCAGCAG

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCCAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIGURE 25B

```

601  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+-----+ 660
      GTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

      AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
661  -----+-----+-----+-----+-----+-----+ 720
      TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A      K  S  L  S  L  S  P  G  K  G  G  G  G  G  C  T  T  H  W  G  -

              BamHI
              |
      TTCACCCTGTGCTAATGGATCCCTCGAG
721  -----+-----+-----+-----+-----+ 748
      AAGTGGGACACGATTACCTAGGGAGCTC

a      F  T  L  C  *
```

FIGURE 26A

NdeI
|
CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT
1 -----+-----+-----+-----+-----+ 60
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA

a M C T T H W G F T L C G G G G G D K G -

61 GGAGGCGGTGGGGACAAAACCTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG
-----+-----+-----+-----+-----+ 120
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGTTGACTTGAGGACCCC

a G G G G D K T H T C P P C P A P E L L G -

121 GGACCGTCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACC
-----+-----+-----+-----+-----+ 180
CCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG

a G P S V F L F P P K P K D T L M I S R T -

181 CCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
-----+-----+-----+-----+-----+ 240
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG

a P E V T C V V V D V S H E D P E V K F N -

241 TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
-----+-----+-----+-----+-----+ 300
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG

a W Y V D G V E V H N A K T K P R E E Q Y -

301 AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
-----+-----+-----+-----+-----+ 360
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG

a N S T Y R V V S V L T V L H Q D W L N G -

361 AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
-----+-----+-----+-----+-----+ 420
TTCTCATGTTCACGTTCAGAGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG

a K E Y K C K V S N K A L P A P I E K T I -

421 TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
-----+-----+-----+-----+-----+ 480
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA

a S K A K G Q P R E P Q V Y T L P P S R D -

481 GAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
-----+-----+-----+-----+-----+ 540
CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTG

a E L T K N Q V S L T C L V K G F Y P S D -

541 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCC
-----+-----+-----+-----+-----+ 600
TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGGGAGGG

a I A V E W E S N G Q P E N N Y K T T P P -

FIGURE 26B

```

601  GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC GTGGACAAGAGCAGG 660
      -----+-----+-----+-----+-----+-----+
      CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a      V L D S D G S F F L Y S K L T V D K S R -

      TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661  -----+-----+-----+-----+-----+-----+ 720
      ACCGTCGTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a      W Q Q G N V F S C S V M H E A L H N H Y -

                                     BamHI
                                     |
      ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721  -----+-----+-----+-----+-----+ 763
      TCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a      T Q K S L S L S P G K *
```